

Postweaning Multisystemic Wasting Syndrome (PMWS) Clone 412

ACCAGCGCACTTCGGCAGCGGCAGCACCTCGGCAGCACCTCAGCAGCAACATGCCAGCAAGAAGAATGGA  
AGAAGCGGACCCCAACCACATAAAAGGTGGGTGTTACGCTGAATAATCCTTCCGAAGACGAGCGCAAGAA  
AATACGGGAGCTCCCAATCTCCCTATTTGATTATTTTATTGTTGGCGAGGAGGGTAATGAGGAAGGACGAA  
CACCTCACCTCCAGGGGTTTCGCTAATTTTGTGAAGAAGCAAACCTTTTAATAAAGTGAAGTGGTATTTGGGT  
GCCCGCTGCCACATCGAGAAAGCCAAAGGAAGTATCAGCAGAATAAAGAATATTGCAGTAAAGAAGGCAA  
CTTACTTATTGAATGTGGAGCTCCTCGATCTCAAGGACAACGGAGTGACCTGTCTACTGCTGTGAGTACCT  
TGTGAGAGAGCGGGATTCTGGTGACCGTTGCAAAGCAGCACCTGTAAACGTTTGTCAAAAATTTCCGCGGG  
CTGGCTGAACTTTTGAAAGTGAGCGGGAATGCAAAGCGTGATTGGAACCAATGTACACTTCATTGT  
GGGGCCACCTGGGTGTGGTAAAGCAAATGGGCTGCTAATTTTGCAAACCGGAAACCACATACTGGAAC  
CACCTAAAAACAAGTGGTGGGATGGTTACCATGGTGAAAAAGTGGTGTATTGATGACTTTTATGGCTGG  
CTGCCGTGGGATGATCTACTGAGACTGTGTGATCGATATCCATTGACTGTAAAACTAAAGGTGGAAGTGT  
ACCTTTTTTTGGCCCGCAGTATTCTGATTACCAGCAATCAGACCCCGTTGGAATGGTACTCCTCAACTGCTG  
TCCCAGCTGTAGAAGCTCTCTATCGGAGGATTACTTCCTTGGTATTTTGGAAGAATGCTACAAAACAATCC  
ACGGAGGAAGGGGGCCAGTTCGTACCCCTTTCCCCCATGCCCTGAATTTCCATATGAAATAAATTAAGT  
AGTCTTTTTTATCACTTCGTAATGGTTTTTATTATTATTTAGGGTTCAAGTGGGGGGTCTTTAAGATTAA  
ATTCTCTGAATTGTACATACATGGTTACACGGATATTGTAGTCCTGGTCGTATTTACTGTTTTTCGAACGCA  
GTGCCGAGGCCTACGTGGTCCACATTTCCAGAGGTTTGTAGCCTCAGCCAAAGCTGATTCCTTTTGTATT  
TGGTTGGAAGTAATCAATAGTGGAGTCAAGAACAGGTTTGGGTGTGAAGTAACGGGAGTGGTAGGAGAAGG  
GTTGGGGGATTGTATGGCGGGAGGAGTAGTTTACATATGGGTATAGGTTAGGGCTGTGGCCTTTGTACA  
AAGTTATCATCTAAAATAACAGCAGTGGAGCCCACTCCCCTATCACCTGGGTGATGGGGGAGCAAGGCCA  
GAATTCACCTTAACCTTTCTTATTCTGTAGTATTCAAAGGGTATAGAGATTTTGTGGTCCCCCTCCCG  
GGGGAACAAAGTCGTCAATTTTAAATCTCATGTCCACCGCCAGGAGGGCGTTGTGACTGTGGTACGC  
TTGACAGTATATCCGAAGGTGCGGGAGAGGCGGGTGTGAAGATGCCATTTTCTTCTCAACGGTAGCG  
GTGGCGGGGGTGGACGAGCCAGGGGCGGCGGAGGATCTGGCCAAGATGGCTGCGGGGGCGGTGTCTTC  
TTCTGCGGTAACGCCTCCTTGGATACGTATAGCTGAAAACGAAAGAAGTGCCTGCTGTAGTATT

FIG. 1

5069750-121697

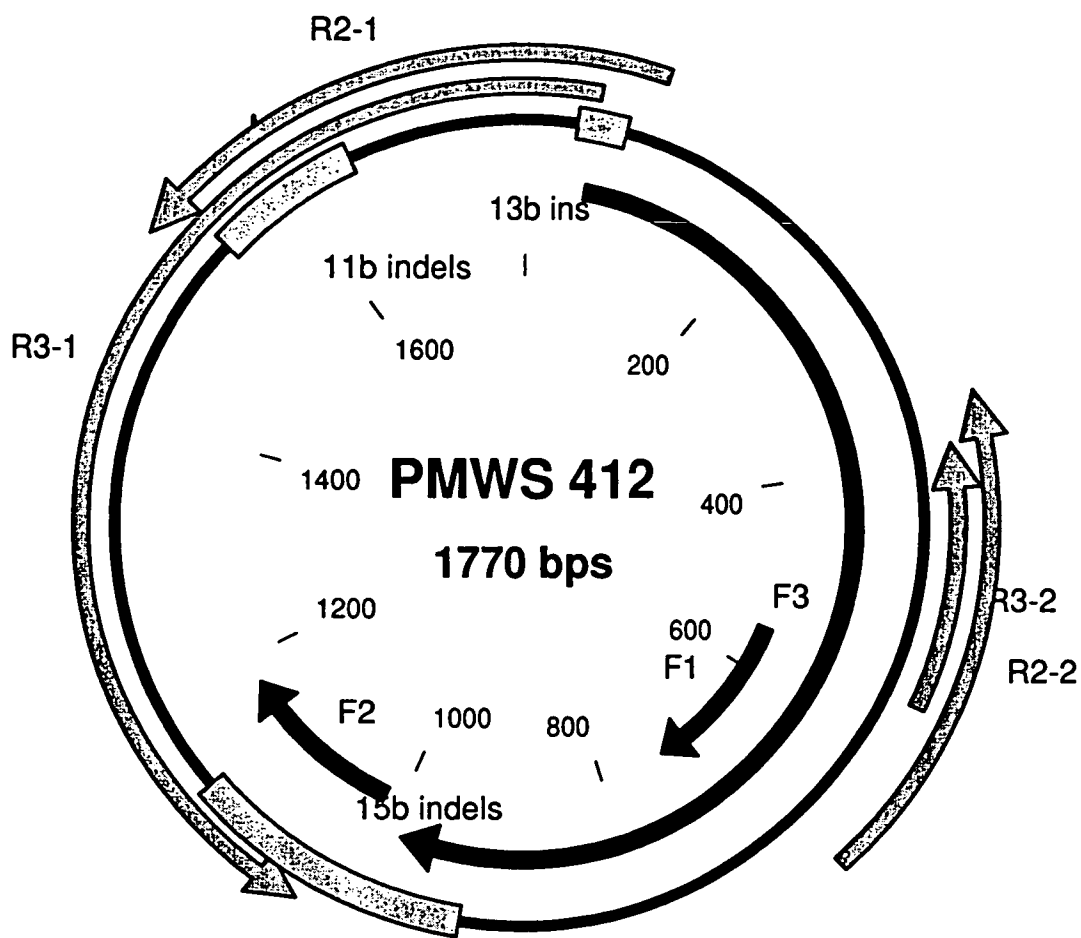


FIG. 2

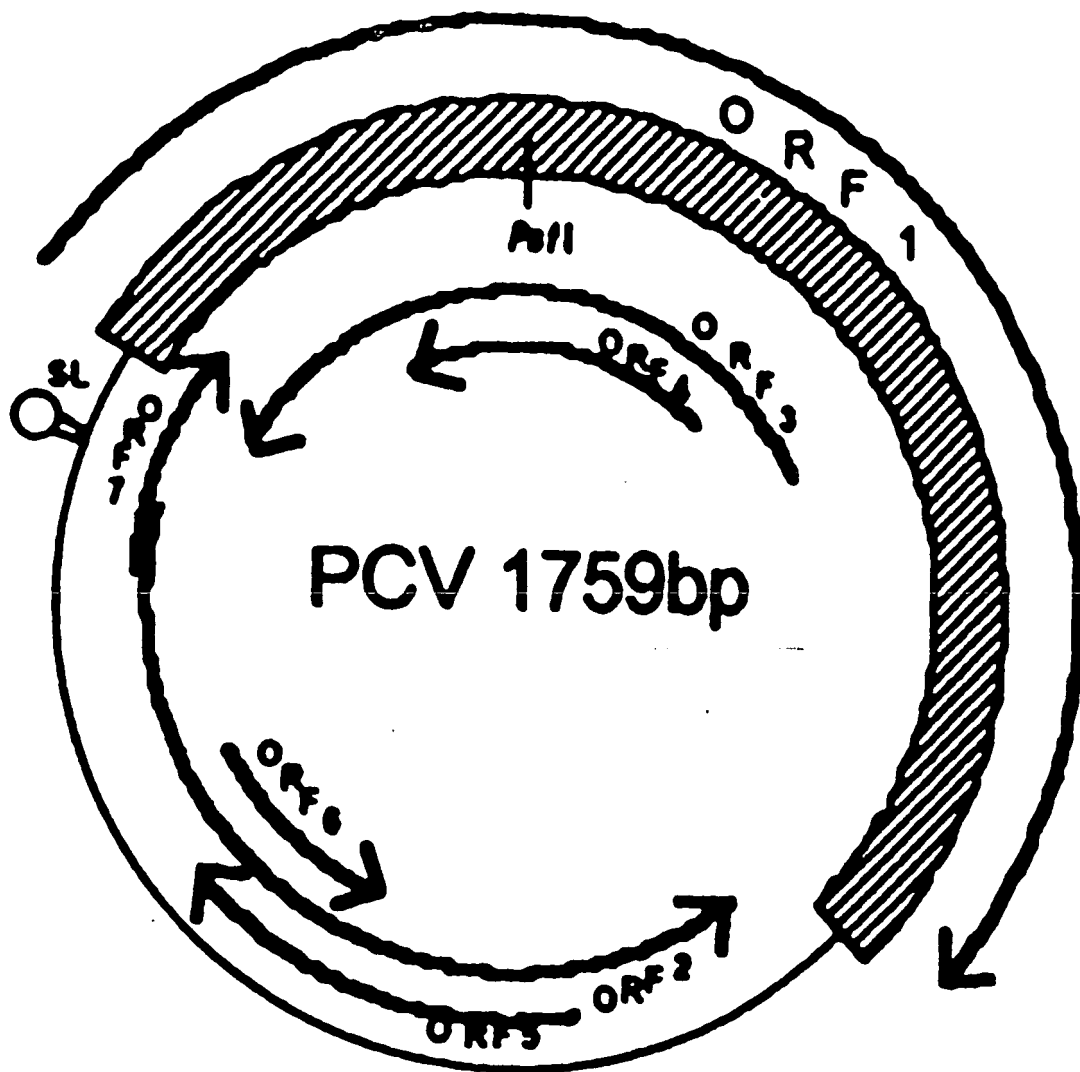


FIG. 3



	610	620	630	640	650	660
412	CTGCTAATTTTGCAAACCCGGAACCCACATACTGGAAACCACTAAAAACAAGTGGTGGG					
	:	:	:	:	:	:
PCV	CCCGTAATTTTGCTGAGCCTAGGGACACCTACTGGAAGCCTAGTAGAAATAAGTGGTGGG					
	590	600	610	620	630	640
	670	680	690	700	710	720
412	ATGGTTACCATGGTGAAAAAGTGGTTGTTATTGATGACTTTTATGGCTGGCTGCCGTGGG					
	:	:	:	:	:	:
PCV	ATGGATATCATGGAGAAGAAGTTGTTGTTTGGATGATTTTATGGCTGGTTACCTTGGG					
	650	660	670	680	690	700
	730	740	750	760	770	780
412	ATGATCTACTGAGACTGTGTGATCGATATCCATTGACTGTAAAACTAAAGGTGGAAC TG					
	:	:	:	:	:	:
PCV	ATGATCTACTGAGACTGTGTGACCGGTATCCATTGACTGTAGAGACTAAAGGGGTACTG					
	710	720	730	740	750	760
	790	800	810	820	830	840
412	TACCTTTTTTGGCCCGCAGTATTCTGATTACCAGCAATCAGACCCCGTTGGAATGGTACT					
	:	:	:	:	:	:
PCV	TTCCTTTTTTGGCCCGCAGTATTCTGATTACCAGCAATCAGGCCCCCGAGGAATGGTACT					
	770	780	790	800	810	820
	850	860	870	880	890	900
412	CCTCAACTGCTGTCCAGCTGTAGAAGCTCTCTATCGGAGGATTACTTCCCTGGTATTTT					
	:	:	:	:	:	:
PCV	CCTCAACTGCTGTCCAGCTGTAGAAGCTCTCTATCGGAGGATTACTACTTTGCAATTTT					
	830	840	850	860	870	880
	910	920	930	940	950	
412	GGAAGAATGCTACAAAACAATCCACGGAGGAA--GGGGCCAGTTCGTACCCCTTTCCC					
	:	:	:	:	:	:
PCV	GGAAGACTGCTGGAGAACAATCCACGGAGGTACCCGAAGCCGATTGAAGCAGTGGACC					
	890	900	910	920	930	940
	960	970	980	990	1000	1010
412	CCCCATGCCCTGAATTCCCATATGAAATAAATTACTGAGTCTTTTTT--ATCACTTCGT					
	:	:	:	:	:	:
PCV	CACCCCTGTGCCCTTTTCCCATATAAAATAAATTACTGAGTCTTTTTTGTATCACATCGT					
	950	960	970	980	990	1000
	1020	1030	1040	1050	1060	1070
412	AATGGTTTTTTATTATTCATTTAGGGTTCAAGTGGGGGTCTTTAAGATTAAATTCTCTGA					
	:	:	:	:	:	:
PCV	AATGGTTTTTTATT-TTTATTTA---TTTA---GAGGGTCTTTTAGGATAAATTCTCTGA					
	1010	1020	1030	1040	1050	
	1080	1090	1100	1110	1120	1130
412	ATTGTACATACATGGTTACACGGATATTGTAGTCCTGGTC-GTATTACTGTTTTCGAAC					
	:	:	:	:	:	:
PCV	ATTGTACATAAATAGTCAGCCTTACCACATAATTTTGGGCTGTGGCTGCA-TTTTGGAGC					
	1060	1070	1080	1090	1100	1110
	1140	1150	1160	1170	1180	1190
412	GCAGTGCCGAGGCCTACGTGGTCCACATTTCCAGAGGTTGTAGCCTCAGCCAAAGCTGA					
	:	:	:	:	:	:
PCV	GCATAGCCGAGGCCTGTGTGCTCGACATTGGTGTGGGTATTTAAATGGAGCCACAGCTGG					
	1120	1130	1140	1150	1160	1170

FIG. 4B



412 f3 314 aa vs.  
pcv f2-1 312 aa  
scoring matrix: , gap penalties: -12/-2  
83.5% identity; Global alignment score: 1855

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      10      20      30      40      50      60
MPSKKNRSGPQPHKRWVFTLNNPSEDERKKIRELPISLFDYFIVGEEGNEEGRTPHLQG
.....
MPSKK---SGPQPHKRWVFTLNNPSEEEKNKIRELPISLFDYFVCGEEGLEEGRTPHLQG
      10      20      30      40      50

      70      80      90     100     110     120
FANFVKKQTFNKVKWYLGARCHIEKAKGTDQQNKEYCSKEGNLLIECGAPRSQGQRSDLS
.....
FANFAKKQTFNKVKWYFGARCHIEKAKGTDQQNKEYCSKEGHILIECGAPRNQGKRSDLS
     60      70      80      90     100     110

     130     140     150     160     170     180
TAVSTLLESGILVTVAQHVPVTFVKNFRGLAELLKVSQKMQKRDWKTNVHFIVGPPGCGK
.....
TAVSTLLETGSLVTVAEQFPVTYVRNFRGLAELLKVSQKMQQRDWKTAVHVIVGPPGCGK
    120     130     140     150     160     170

     190     200     210     220     230     240
SKWAANFANPETTYWKPPKNKWWDGYHGEKVVVIDDFYGWLPWDDLRLCDRYPLTVKTK
....
SQWARNFAEPRDTYWKPSRNKWWDGYHGEEVVVLDLDFYGWLPWDDLRLCDRYPLTVETK
    180     190     200     210     220     230

     250     260     270     280     290
GGTVPFLARSILITSNQTPLEWYSSTAVPAVEALYRRITSLVFWKNATKQSTE-EGGQFV
.....
GGTVPFLARSILITSNQAPQEWYSSTAVPAVEALYRRITTLQFWKTAGEQSTEVPEGRFE
    240     250     260     270     280     290

    300     310
    TLSPPCPEFPYEINY
    .....
    AVDPPCALFPYKINY
    300     310

```

FIG. 5A

60069750-121697

412 r3-1

pcv r1-1

scoring matrix: , gap penalties: -12/-2

58.9% identity; Global alignment score: 999

261 aa vs.

231 aa

```

      10      20      30      40      50      60
MLLLRCCRGAAAAEVRWYYSSALLSFSAMTYPRRRYRRRRHRPRSHLGQILRRRPWLVHP
      :                               ::::::::::::::::::::::
-----W-----PRRRYRRRRTRPRSHLGNIILRRRPYLAHP
                        10      20      30

      70      80      90      100     110
--RHRYRWRRKNGIFNTRLSTFGYTVKRTTVTTPSWAVDMMRFKIDDFVPPGGGTNKIS
      :::::::::::::: : :: . :: :::::::::: ::::::::::
AFRNRYRWRRKTGIFNSRLSTEFVLTIK-GGYSQPSWNVNLYLKFNIGQFLPPSGGTNPLP
      40      50      60      70      80

120      130      140      150      160      170
IPFEYYRIRKVKVEFWPCSPITQGRGVGSTAVILDDNFVTKATALTYDPYVNYSSRHTI
:::::::::::: :::: :::::::::::::::::::::: :::: : ::::::::::::::
LPFQYYRIRKAKYEFYPRDPITSNQRGVGSTVVILDANFVTPSTNLAYDPYINYSSRHTI
90      100      110      120      130      140

180      190      200      210      220      230
PQFYSYHSRYFTPKPVLDSTIDYFQPNKRNLWLRLQTSNVDHVGGLTAFENSKYDQD
:::::::::::: :::::::::::::::::::::: :::::::::: ::::: ::
RQPFYYSRYFTPKPELDQTIDWFHPNNKRNLWLHLNHTNVEHTGLGYALQNAATAQN
150      160      170      180      190      200

240      250      260
YNIRVTMYVQFREFNLKDPPLEP
: :::::::::::::: :::: :
YVVRLLTIYVQFREFILKDP-LNK
210      220      230

```

FIG. 5B

469750-121697



412 r3-2

pcv r2-2

scoring matrix: , gap penalties: -12/-2

40.9% identity; Global alignment score: 178

59 aa vs.

115 aa

```

      10      20      30      40      50
MKCTLVFQSRFCIFPLTFKSSASPRKFLTNVTGCCFATVTRIPLSNKVLTAVDRSLRCP-
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
- MTCTAVFQSRCCIFPLTFKSSASPRKFLTYVTGNCSATVTKDPVSKRVLTAVDRSLRFPW
      10      20      30      40      50      60

-----

- FRGAPHSISMWPSLLQYSLFCWSVPFAFSMWQRAPKYHFTLLKVCFLAKFANPWR
      70      80      90     100     110
```

**FIG. 5C**

60069750-121697

412 r2-2

pcv r1-2

scoring matrix: , gap penalties: -12/-2

29.1% identity; Global alignment score: 157

104 aa vs.

206 aa

```

      10      20      30      40      50      60
MVTIPPLVFRWFPVCGFRVCKISSPFAFTTPRWPHNEVYIGFPITLLHFP AHFQKFSQPA
.....  .:  .:  .....  :  :  .....
- MISIPPLISTRLPVGVPRLSKITGPLALPTTGRAHYDVYSCLPITLLHLP AHFQKFSQPA
      10      20      30      40      50      60

      70      80      90      100
EIFDKRYRVLLCNGHQNPALQQGTHSSRQVTPLSLRSRSSTFNK-----
::  :::  ::  .:  :  .....  :  :  .....
- EISHIRYRELLGYSHQRPRLQKGTHSSRQVAALPLVPRSSTLDKYVAFFTAVFFILLVGS
      70      80      90      100      110      120

-----

- FRFLDVAAGTKIPLHLVKSLLLSKIRKPLEVRSSTLFQTFLSANKIIKKGDWKLPHYFVFL
      130      140      150      160      170      180

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- LLGRIIKGEHPPLMGLRAAFLAWHFH
      190      200
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FIG. 5D

60069750 121697



PCV	ATTGTACATAAATAGTCAAGCCTTACCACATAAATTTGGGCTGTGGCTGCA - TTTTGGAGCGCATAGCCGAGGCCCTGTGTGCTCGACATTTGCTGTGGGTATTTAAATGGAGCCACAGCTGG	C G T CA GG TATTG G CC T - ATT A TG C A GT AC G C TCCAGA T G GCCTC A A	C G T CA GG TATTG G CC T - ATT A TG C A GT AC G C TCCAGA T G GCCTC A A	C G T CA GG TATTG G CC T - ATT A TG C A GT AC G C TCCAGA T G GCCTC A A	C G T CA GG TATTG G CC T - ATT A TG C A GT AC G C TCCAGA T G GCCTC A A	
412						
9741						
B9						
B1						
B4						
PCV	TTTCTTTTATTATTGGGTGGAACCAATCAATTTGTTGGTCCAGCTCAGGTTTGGGGGTGAAGTACCTGGAGTGGTAGGTAAGGGCTGCCTTATGGTGTGGCGGAGGAGTAGTTAATA	C G T GT A GGA A AA T A G AG T GGG T A T C	C G T GT A GGA A AA T A G AG T GGG T A T C	C G T GT A GGA A AA T A G AG T GGG T A T C	C G T GT A GGA A AA T A G AG T GGG T A T C	C G T GT A GGA A AA T A G AG T GGG T A T C
412						
9741						
B9						
B1						
B4						
PCV	TAGGGGTATAGGCCAAGTTGGTAGGGGGTTACAAAGTTGGCATCCAAAGATAACAACAGTGGAGCCCAACACCCTCTTTGATTAGAGGTGATGGGCTCTCTGGGGTAAATTCATATTTA	T TT G GCT CTTTT AT T A G C T C A C CCCTG GAG AA CC G ACC	T TT G GCT CTTTT AT T A G C T C A C CCCTG GAG AA CC G ACC	T TT G GCT CTTTT AT T A G C T C A C CCCTG GAG AA CC G ACC	T TT G GCT CTTTT AT T A G C T C A C CCCTG GAG AA CC G ACC	T TT G GCT CTTTT AT T A G C T C A C CCCTG GAG AA CC G ACC
412						
9741						
B9						
B1						
B4						
PCV	GCCTTTCTAATACGGTAGTATTGGAAGGTAGGGGTAGGGGTGGGGGAGGAACTGGCCGCTGATGGCGGAGGAACTGGCCGATGTTGAAATTTGAGTAGTTAAACATTTCCAAGATGGC - - TGCGAGT	A T T T CA G TA AG TTTT C C CCC A CA G C T A T A C C TCAT CC CGC G G GT T C	A T T T CA G TA AG TTTT C C CCC A CA G C T A T A C C TCAT CC CGC G G GT T C	A T T T CA G TA AG TTTT C C CCC A CA G C T A T A C C TCAT CC CGC G G GT T C	A T T T CA G TA AG TTTT C C CCC A CA G C T A T A C C TCAT CC CGC G G GT T C	A T T T CA G TA AG TTTT C C CCC A CA G C T A T A C C TCAT CC CGC G G GT T C
412						
9741						
B9						
B1						
B4						
PCV	ATCCTCCTTTT - ATGTGAGTACAAATTCGTAGAAAGGCGGGAATTCGAAGATACCCGCTTTTCGGCGCCATCTGTAAACGGTTTCTGAAGCGGGG - TGTGCCAAATATGGTCTTCTCCG	G GG A GC G CA ATA C G GGTGCGG G TG G AT T C TT T A G G - - - - - G GA G GCC G G GG GG	G GG A GC G CA ATA C G GGTGCGG G TG G AT T C TT T A G G - - - - - G GA G GCC G G GG GG	G GG A GC G CA ATA C G GGTGCGG G TG G AT T C TT T A G G - - - - - G GA G GCC G G GG GG	G GG A GC G CA ATA C G GGTGCGG G TG G AT T C TT T A G G - - - - - G GA G GCC G G GG GG	G GG A GC G CA ATA C G GGTGCGG G TG G AT T C TT T A G G - - - - - G GA G GCC G G GG GG
412						
9741						
B9						
B1						
B4						
PCV	GAGGATGTTTCCAAAGATGGCTGCGGGGGGGTCTTCTTCTTCGGGTAAAGCCCTCCTTGGCCACGTCATCCTATATAAAGTGAAGAGTGGCGTGTCTGA - GTATT	C GG TGT AT AGCTG C- - - - A	C GG TGT AT AGCTG C- - - - A	C GG TGT AT AGCTG C- - - - A	C GG TGT AT AGCTG C- - - - A	C GG TGT AT AGCTG C- - - - A
412						
9741						
B9						
B1						
B4						

FIG. 6B